

GenCore version 4.5
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Om protein - protein search, using sw model

Run on: August 28, 2002, 17:32:27 ; Search time 37.53 Seconds
(without alignments)
637.523 Million cell updates/sec

Title: US-09-502-984B-37
Perfect score: 1284
Sequence: 1 KFESKAALLAARGPEELLCF RKNERLEEEVERLKQLVGER 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:71:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

ZUHUR

erythropoietin receptor precursor - human

C;Species: Homo sapiens (man)

C;Date: 12-Feb-1993 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999

C;Accession: A43799; A60160; A49824; A55958; A55980; I52563

R;Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.

Blood 76, 31-35, 1990

A;Title: Human erythropoietin receptor: cloning, expression, and biologic characterization

A;Reference number: A43799; MUID:90304340

A;Cross-references: GB:M60459; NID:gil82244; PIDN:AAA52403.1; PID:gil82245

R;Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.

Blood 76, 24-30, 1990

A;Title: The gene for the human erythropoietin receptor: analysis of the coding sequence

A;Reference number: A60160; MUID:90304334

A;Accession: A60160

A;Status: not compared with conceptual translation

A;Molecule type: mRNA; DNA

A;Residues: 1-101,'R','103-188,'RP','191-243,'E','245-508 <WIN>

R;Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.

Blood 78, 2548-2556, 1991

A;Title: Cloning of the human erythropoietin receptor gene.

A;Reference number: A49824; MUID:92399733

A;Accession: A49824

A;Molecule type: DNA

A;Residues: 1-508 <NOG>

A;Cross-references: GB:S45332; NID:9255496; PIDN:AB23271.1; PID:g255497

A;Experimental source: placenta

A;Title: Sequence extracted from NCBI backbone (NCBIN:113293, NCBIP:113294)

A;Reference number: A43958; MUID:91372359

A;Accession: A55280

A;Molecule type: mRNA

A;Residues: 1-508 <EUR>

R;Penny, L.A.; Forget, B.G.

Genomics 11, 974-980, 1991

A;Title: Genomic organization of the human erythropoietin receptor gene.

A;Reference number: A55280; MUID:92147143

A;Accession: A55280

A;Molecule type: DNA

A;Residues: 1-17;381-387,'LLEQQQDA',391-395;504-508 <PNP>

A;Note: sequence modified after extraction from NCBI backbone

A;Note: the authors translated the codon GAT for residue 31 as B

A;Note: an insert compared to other published sequences is considered by authors as 1

A;Title: Cloning of the gene encoding the human erythropoietin receptor.

Env/v-mpl fusion p

A; Reference number: 152563; MUID:92399734
 A; Accession: I52563
 A; Status: translated from GB/EMBL/DBBJ
 A; Molecule type: DNA
 A; Cross-references: GB:M76595; NID:9182147; PID:AAA52393.1; PID:9553281
 C; Genetics:
 A; Gene: GDB:EPOR
 A; Cross-references: GDB:125242; OMIM:133171
 A; Map position: 19p13.3-19q13.2
 A; Introns: 39/1; 84/2; 143/1; 195/3: 247/1; 276/2; 305/3
 C; Superfamily: erythropoietin receptor; cytokine receptor homology
 C; Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-508/Product: erythropoietin receptor #status predicted <MAT>
 F; 52-230/Domain: extracellular #status predicted <EXT>
 F; 52-239/Domain: cytokine receptor homology <CRS>
 F; 253-237/Region: WSXWS motif
 F; 251-272/Domain: transmembrane #status predicted <TM>
 F; 52-62; 91-107/disulfide bonds: #status predicted <INT>
 F; 76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.3%; Score 877.5; DB 1; Length 507;
 Best Local Similarity 78.2%; Pred. No. 1 8e-68;
 Matches 165; Conservative 23; Mismatches 22; Indels 1; Gaps 1;
 C; Residues: 1-96 <RES>
 A; Cross-references: GDB:125242; OMIM:133171
 A; Map position: 19p13.3-19q13.2
 A; Introns: 39/1; 84/2; 143/1; 195/3: 247/1; 276/2; 305/3
 C; Superfamily: erythropoietin receptor; cytokine receptor homology
 C; Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-508/Product: erythropoietin receptor #status predicted <MAT>
 F; 52-230/Domain: extracellular #status predicted <EXT>
 F; 52-239/Domain: cytokine receptor homology <CRS>
 F; 253-237/Region: WSXWS motif
 F; 251-272/Domain: transmembrane #status predicted <TM>
 F; 52-62; 91-107/disulfide bonds: #status predicted <INT>
 F; 76/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 2
 A46713 erythropoietin receptor precursor - rat
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C; Accession: A46713
 R; Masuda, S.; Nagao, M.; Takahashi, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki, J.; Biol. Chem., 268, 11208-11216, 1993
 A; Title: Functional erythropoietin receptor of the cells with neural characteristics. Co
 A; Reference number: A46713; MUID:93266574
 A; Accession: A46713
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-24 <RES>
 A; Cross-references: GB:M62360; NID:919319; PID:AAA37582.1; PID:9193200
 C; Superfamily: erythropoietin receptor; cytokine receptor homology
 C; Keywords: cytokine receptor; transmembrane protein
 F; 52-238/Domain: cytokine receptor homology <CRS>

RESULT 3
 S14081 erythropoietin receptor - mouse
 C; Species: Mus musculus (house mouse)
 C; Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C; Accession: S14081; I49653
 R; Kuramochi, S.; Ikawa, Y.; Todokoro, K.
 J. Mol. Biol., 216, 567-575, 1990
 A; Title: Characterization of murine erythropoietin receptor genes.
 A; Reference number: S13249; MUID:91080149
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-265 <KUR>
 R; LaCombe, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.
 J. Biol. Chem., 266, 6952-6956, 1991
 A; Title: Spike focus-forming virus long terminal repeat insertional activation of th
 A; Reference number: I49653; MUID:91201346
 A; Accession: I49653
 A; Status: preliminary; translated from GB/EMBL/DBBJ
 A; Molecule type: DNA
 A; Residues: 1-24 <RES>
 A; Cross-references: GB:M62360; NID:919319; PID:AAA37582.1; PID:9193200
 C; Superfamily: erythropoietin receptor; cytokine receptor homology
 C; Keywords: cytokine receptor; transmembrane protein
 F; 52-238/Domain: cytokine receptor homology <CRS>

Query Match 68.2%; Score 875.5; DB 2; Length 265;
 Best Local Similarity 77.1%; Pred. No. 1 2e-68;
 Matches 165; Conservative 22; Mismatches 26; Indels 1; Gaps 1;
 C; Residues: 1-507 <MAS>
 A; Experimental source: PC12 and erythroid cells
 A; Cross-references: GB:D13566; NID:9286209; PID:BA02761.1; PID:9286210
 A; Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBIP:132813)
 C; Superfamily: erythropoietin receptor; cytokine receptor homology
 C; Keywords: cytokine receptor; glycoprotein; transmembrane protein
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-507/Product: erythropoietin receptor #status predicted <MAT>
 F; 25-249/Domain: extracellular #status predicted <EXT>
 F; 250-271/Domain: transmembrane #status predicted <TM>
 F; 250-507/Domain: intracellular #status predicted <INT>
 F; 75/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 4
 A32385 erythropoietin receptor precursor, membrane-bound form - mouse

C;Species: Mus musculus (house mouse)
 C;Accession: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999
 R;Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
 Mol. Cell. Biol. 11, 5527-5533, 1991
 A;Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
 A;Reference number: A41686; MUID:92017832
 A;Accession: A41686
 A;Molecule type: mRNA
 A;Residues: 1-507 <HIN>
 A;Cross-references: GB:MS5388; NID:9237036; PIDN:AA20029.1; PID:9237037
 A;Experimental source: murine erythroleukemia (MEL) cell line F5-5
 R;D'Andrea, A.D.; Ledish, H.F.; Wong, G.G.
 Cell 57, 277-285, 1989
 A;Title: Expression cloning of the murine erythropoietin receptor.
 A;Reference number: A32385; MUID:89195288
 A;Accession: A32385
 A;Molecule type: mRNA
 A;Residues: 1-507 <DNA>
 A;Cross-references: GB:J04843; NID:9193090; PIDN:AAA37571.1; PID:9309219
 A;Experimental source: murine erythroleukemia (MEL) cells, subclone 745
 R;Kuramochi, S.; Ikeda, Y.; Todokoro, K.
 J. Mol. Biol. 216, 567-575, 1990
 A;Title: Characterization of murine erythropoietin receptor genes.
 A;Reference number: S13249; MUID:91080149
 A;Accession: S13249
 A;Molecule type: DNA; mRNA
 A;Residues: 1-507 <KUR>
 A;Cross-references: EMBL:X53081; NID:950861; PIDN:CAA37248.1; PID:950862
 A;Experimental source: murine erythroleukemia K-1 cells
 C;Genetics:
 A;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
 C;Superfamily: erythropoietin receptor; cytokine receptor homology
 C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-507/Product: erythropoietin receptor #status predicted <MAT>
 F;25-249/Domain: extracellular #status predicted <EXT>
 F;250-238/Domain: cytokine receptor homology <CRS>
 F;250-271/Domain: transmembrane #status predicted <TM>
 F;277-507/Domain: intracellular #status predicted <INT>
 F;52-62, 90-106/Disulfide bonds: #status predicted
 F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 67.7%; Score 869.5; DB 1; Length 507;
 Best Local Similarity 77.7%; Pred. No. 9e-68;
 Matches 164; Conservative 22; Mismatches 24; Indels 1; Gaps 1;
 Result 5
 Query 1 KFESKAALLAARGPPEELCPTERLEDVCFEEAASAGVVERGNEFERSFOEDEDPWKLCRL 60
 Db 34 KEFSKALLAARGPSEBLCLCTQRLEDVCFEEAASSGM-DFTNSFSYQLEGESRKSCSL 92
 Query 61 HQAPTAARGAIRFWCSLPTADTSFVPLERLTAAAGPAPRHRVIIHNEVVLDAVGVA 120
 Db 93 HQAPTVRGSVRFCSLPTADTSFVPLERLTAAAGPAPRHRVIIHNEVVLDAVGVA 152
 Query 121 RLADESGHVVIRWLPPPETPMTHIRPFELDISAGNGAGSIVQRVLEGRTECVLSNLGR 180
 Db 153 RRAEGGSHVWLSPPGAPMTTHIREVDSAGNRAGGTQREVELEGTECVLSNLRRG 212
 Query 181 TRITAVRARAAKEPREGFGFNSAWSEVSLT 211.
 Db 213 TRYTFAVRARMAPEPSPSGFWNSAWSEPAASLT 243
 Result 5
 Query Match 12.8%; Score 164; DB 2; Length 626;
 Best Local Similarity 23.5%; Pred. No. 2.6e-06;
 Matches 61; Conservative 34; Mismatches 105; Indels 60; Gaps 8;
 Result 6
 Query 4 SKAALLAARGPPEELCPTERLEDVCFEEAASAGVVERGNEFERSFOEDEDPWKLCRLHQA 63
 Db 18 SQDVFLALGTEPLNCFSQIFEDLFCFWDEEEA-PSGTYQOLLYARYGRKPRACPLSQ 75
 Query 64 PTARGAIRFWCSLPTAD-TSFVPLERLTAAAGPAPRHRVIIHNEVVLDAVGVA 121
 Db 83 SVPTFGTRRYVQCPAQDEOVRFLFPFLWVKVNSLNOTLJQRLVFLFVSDVGLPAPPRVIKAR 142
 Query 122 LADESGHVVIRW-LPPEPPTMTHIRPFELDISAGNGAGSIVQRVLEGRTECVLSNLGR 170
 Db 143 GGSQPEBLQIWEAPE--ISDFLRHLLRGPTDSNATAPSV--IQLISTERCPCPLW 198
 Query 171 ECVLISNRGRTRITIAVARMAMEPSFG 197
 Db 199 MPNPVPUQLDQPCVHHTASQPHGPAFPFLVKGGSCLVSGLOASKSYWQLRSQPGCVSLR 258
 Query 198 GFWSANSEPVSL 209
 Db 259 GSWPGPMSFPVTV 270
 Result 6
 Query Match 13.3%; Score 171; DB 2; Length 625;
 Best Local Similarity 24.6%; Pred. No. 6.4e-07;
 Matches 62; Conservative 33; Mismatches 105; Indels 52; Gaps 8;
 Result 7
 Query 4 SKAALLAARGPPEELCPTERLEDVCFEEAASAGVVERGNEFERSFOEDEDPWKLCRLHQA 63
 Db 25 SQDVFLALGTEPLNCFSQIFEDLFCFWDEEEA-PSGTYQOLLYARYGRKPRACPLSQ 82
 Query 64 PTARGAIRFWCSLPTAD-TSFVPLERLTAAAGPAPRHRVIIHNEVVLDAVGVA 121
 Db 83 SVPTFGTRRYVQCPAQDEOVRFLFPFLWVKVNSLNOTLJQRLVFLFVSDVGLPAPPRVIKAR 142
 Query 122 LADESGHVVIRW-LPPEPPTMTHIRPFELDISAGNGAGSIVQRVLEGRTECVLSNLGR 170
 Db 143 GGSQPEBLQIWEAPE--ISDFLRHLLRGPTDSNATAPSV--IQLISTERCPCPLW 198
 Query 171 ECVLISNRGRTRITIAVARMAMEPSFG 197
 Db 199 MPNPVPUQLDQPCVHHTASQPHGPAFPFLVKGGSCLVSGLOASKSYWQLRSQPGCVSLR 258
 Result 7
 Query Match 13.3%; Score 171; DB 2; Length 625;
 Best Local Similarity 24.6%; Pred. No. 6.4e-07;
 Matches 62; Conservative 33; Mismatches 105; Indels 52; Gaps 8;
 Result 8
 Query 4 SKAALLAARGPPEELCPTERLEDVCFEEAASAGVVERGNEFERSFOEDEDPWKLCRLHQA 63
 Db 18 SQDVFLALGTEPLNCFSQIFEDLFCFWDEEEA-PSGTYQOLLYARYGRKPRACPLSQ 75
 Query 64 PTARGAIRFWCSLPTAD-TSFVPLERLTAAAGPAPRHRVIIHNEVVLDAVGVA 121
 Db 83 SVPTFGTRRYVQCPAQDEOVRFLFPFLWVKVNSLNOTLJQRLVFLFVSDVGLPAPPRVIKAR 142
 Query 122 LADESGHVVIRW-LPPEPPTMTHIRPFELDISAGNGAGSIVQRVLEGRTECVLSNLGR 170
 Db 143 GGSQPEBLQIWEAPE--ISDFLRHLLRGPTDSNATAPSV--IQLISTERCPCPLW 198
 Query 171 ECVLISNRGRTRITIAVARMAMEPSFG 197
 Db 199 MPNPVPUQLDQPCVHHTASQPHGPAFPFLVKGGSCLVSGLOASKSYWQLRSQPGCVSLR 258
 Result 8
 Query Match 13.3%; Score 171; DB 2; Length 625;
 Best Local Similarity 24.6%; Pred. No. 6.4e-07;
 Matches 62; Conservative 33; Mismatches 105; Indels 52; Gaps 8;

C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C;Accession: BA5268
R;Renauld, J.C.; Duez, C.; Kestmunt, A.; Houssiau, F.; Vytenissove, C.; Van Roost, E.; V;
Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992
A;Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.
A;Reference number: A45268; MUID:92302307
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-522 <RENAME>
A;Cross-references: EMBL:MB4747; NID:9184508; PIDN:AAA58679.1; PID:9184509
C;Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match 8.9%; Score 114.5; DB 2; Length 522;
Best Local Similarity 22.1%; Pred. No. 0.042; Mismatches 61; Conservative 32; Indels 73; Gaps 12; Matches 110; Indels 73; Gaps 12;

Qy 12 RGPPEE--LLCFTTERLEDLVFFEEAASAGVQFGNFSFSFQLEDEPWKLCRILHQAPTARGA 69
Db 47 QGPRSRSTFTCCTNNTRIDCHW-SAPELGQC-----SSPWLFTSNQAPQGTHK 94

Qy 70 IRFWESLPTADDSFVFPLERLTAASG-APRFRHVINEV-----VILLAP 115
Db 95 ---CLIRGSECTTVLPPEAVLVPSDNTTFFHCMMSGREOVSLSVDPPEYERRRHVKLDPP 150

Qy 116 VGLVARLALADESGHVVIRW-LPPETPTSHRFELDISAGNGA-GSVQVELLEGTECV 173
Db 151 SDLQNSIS- SGHCILTWSPALEMTTLYSAFKKQDEAWEQAQHRONIIVGVWLI 208

Qy 174 LSNL-----RGRFRITAVRAR--MAFPSSGGFWSANSEPV----- 208
Db 209 LEAFELDPGFIHEARLRVOMATLEDDWVEERYGWSENSQVPCFQAPORQGPLPPWG 268

Qy 209 -----LITGGGSSRMKELEQKVWELLRK 232

Db 269 WPGNTLIVAVSIFLILLTGPTVYLFLKSPRVKKRIFYQN 304

RESULT 11
S33339

N;Alternate names: growth hormone receptor
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 08-Dec-2000
C;Accession: S33339
R;Adams, T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R.
Mol. Cell. Endocrinol. 73, 135-145, 1990
A;Title: The sheep growth hormone receptor: molecular cloning and ontogeny of mRNA expression
A;Reference number: S33339; MUID:91099608

Query Match 8.6%; Score 110; DB 2; Length 831;
Best Local Similarity 21.5%; Pred. No. 0.19; Mismatches 49; Conservative 39; Indels 46; Gaps 11; Matches 94; Indels 46; Gaps 11;

Qy 14 PEEELCFTERLEDLVFFEEAASAGVQFGNFSFSFQLEDEPWKLCRILHQAPTARGA 73
Db 31 PRIIRCRSLERKETFSCQWPKPGSDGGL-PTNLTLYFSKSEE---EYECPDYRISGPN 85

Qy 74 CSLPTADDSFVFPLERLTA-----SGARFRHVINEVILDAVGVLVARLADEG 127
Db 86 CYFNKNHTSPWTFNTITVATNEIGNSNSDPOY--VDVHSIVORGSPVNLTLETRKSAN 142

Qy 128 --HVVIRWLPPEPTSH--IRFL-----DISANGAGGSVQVELLEGTEC 172
Db 143 IMYLWAKWNSPPLADASSNHLYHIERIKPEKEEWEITISVG----VQ-----TQC 189

Qy 173 VLSNLNRGRTTRITAVRARMAEPSFGFWSANSEPVSLTTGGGSRMK 220
Db 190 KINRLNAGAMRYVWQVRCTL-DP---GEWSENSSERHLIPLSGQSPEK 233

RESULT 13
RGBYA2

N;Alternate names: protein YEL009C
C;Species: Saccharomyces cerevisiae
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 21-Jul-2000
C;Accession: A03605; S50450; A03604
R;Hinnebusch, A.G.
Proc. Natl. Acad. Sci. U.S.A. 81, 6442-6446, 1984
A;Title: Evidence for transnational regulation of the activator of general amino acid
A;Reference number: A03605; MUID:89038531
A;Accession: A03605
A;Molecule type: DNA
A;Residues: 1-281 <HIN>
A;Cross-references: EMBL:K02205; NID:9171581; PIDN:AAA34640.1; PID:9171584
Db 56 CRSEPELETSCHWTGAGNHSILQSQSPVSMQYTRIDQEWBC---PDVYAGNSCYF 110

Qy 77 PTADTSSFVPLERLTAASGAPRFRHVINEVILDAVGVLVARLADES---GHVVI 131
Db 111 NSYSYTSWTPYCILKTSGNGIVD-HKCFSYEDIVOPDPVPGVNWNLNTSLTELHADILV 169

Qy 132 RWLPPPET 139
:| ||| | 139

Proc. Natl. Acad. Sci. U.S.A. 81, 5096-5100, 1984
A:Title: 5' untranslated sequences are required for the translational control of a yeast
A:Reference number: A03604; MUID:8429808
A:Accession: A03604
A:Molecule type: DNA
A:Residues: 1-1238; PGVLVRESCIE' <THI>
A:Cross-references: EMBL:K02649; NID:9171585; PIDN:AAA65521.1; PID:9171586
C:Genetics: SGD:GCN4; MIPS:YEL009C
A:Cross-references: SGD:S0000735; MIPS:YEL009C
A:Map position: 5L
C:Function:
A:Description: transcription regulation
A:Note: required under amino acid starvation conditions for increasing the transcription
C:Superfamily: amino-acid biosynthesis regulatory protein; fos/jun DNA-binding domain homology
C:Keywords: DNA binding; leucine zipper; transcription regulation
F:220-260/Domain: fos/jun DNA-binding domain homology <FJD>
F:253-281/Region: leucine zipper motif

RESULT 14

Query Match	Score	DB	Length	Start	End
Best Local Similarity	84%	1	281	1	281
Matches	69.7%	pred.	No.	0.072	;
Conservative	4	Mismatches	6	Indels	0
N	0	Gaps	0		

Qy 217 RMEILEQKKEKKLNKRREEVERLKVQGER 249
Db 249 RMQKLEDKVEELSKNYHLENEVARLKKLVGGER 281

S32823

somatotropin receptor precursor, major splice form - chicken

N:Alternate names: growth hormone receptor
 N:Contains: somatotropin receptor, short form

C:Species: Gallus gallus (chicken)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Dec-2000

C:Accession: S32823; A9812

R:Burnside, J.; Liou, S.S.; Cogburn, L.A.
 Endocrinology 128, 3183-3192, 1991

A:Title: Molecular cloning of the chicken growth hormone receptor complementary deoxyribonucleic acid
 A:Reference number: S32823; MUID:91243665

A:Accession: S32823
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-608 <BUR>

A:Cross-references: EMBL:M74057; NID:9211810; PIDN:AAA48781.1; PID:9211811
 R:Huang, N.; Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J.
 Mol. Endocrinol. 7, 1391-1398, 1993

A:Title: Overexpression of a truncated growth hormone receptor in the sex-linked dwarf chicken
 A:Reference number: A49812; MUID:94158698

A:Accession: A49812
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-109 <HUA>

A:Cross-references: GB:S68576; NID:9499137; PIDN:AAB29983.1; PID:9499138

A:Experimental source: liver, normal chicken

A:Note: this truncated form is a minor splice form in normal chickens and the major form in transgenic chickens

C:Superfamily: fibronectin type III repeat homology

C:Keywords: alternative splicing; receptor; sex-linked inheritance; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-109/Product: somatotropin receptor, short form #status predicted <SHO>

Query Match 8.3%; Score 107; DB 2; Length 608;
 Best Local Similarity 26.7%; Pred. No. 0.23; Matches 54; Conservative 26; Mismatches 90; Indels 32; Gaps 9;
 Qy 14 PEEILCFTRERLDLVCFFEEAASAGVPGNFSFSFLQ-----EDEPWPKLCRLHQAPTRG 68
 Db 29 PQISKCRSPELETFSQIYID----GKVTSGTIOLYMRSDEDWKEC---PDIY 77
 Qy 69 AIRFWCSLTTADTSSFWPLRILTAASGAFAFRHVRVHNIEVLLDAPVGVLVARLADES-- 126

QY 127 --GHWVIRWLPPPETPMTS--HIRFELDISRNGAGSVORVELLEGRCTECY--LSNLR 178
 | : || | : || | : || | : || | : || | : || | : || | : || | : || | : || | : || |
 137 GIHGDQIVWDPPPTADYQKGWITLEVLEYQKVNET--IWKELLPRLSTVWPLSLK 192
 QY 179 GRTRITIAVARM-AEPSTGGF 199
 | : || | : || | : || | : || | : || | : || | : || | : || | : || | : || |
 Db 193 MGRDYEIRVRSRQRTSEREGEF 214

RESULT 15
 A30304 prolactin receptor 2 precursor - rabbit
 N;Alternate names: prolactin receptor, mammary gland
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-2000
 C;Accession: A30304; A60380
 R;Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusander-Fourt, I.; Petridou, B.; Bou
 Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
 A;Title: Identification and sequence analysis of a second form of prolactin receptor
 A;Reference number: A30304; NUID:89184578
 A;Accession: A30304
 A;Molecule type: mRNA
 A;Residues: 1-616 <EDE>
 A;Cross-references: GB:J04510; NID:9165669; PIDN:AAA31457.1; PID:9165670
 R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A;Title: Purification and partial sequence of the rabbit mammary gland prolactin rec
 A;Reference number: A60380; NUID:91146782
 A;Accession: A60380
 A;Molecule type: protein
 A;Residues: 41-58, 'X', 60-66, 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX'
 A;Note: the amino end of the mature protein was blocked
 C;superfamily: cytokine receptor homology
 C;Keywords: blocked amino end; glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F;36-221/Domain: cytokine receptor homology <CRS>
 F;235-258/Domain: transmembrane #status predicted <TM>
 F;59,104,132,347,359,411/Binding site: carbohydrate (Asn) (covalent) #status predictu

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